

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/687,860
 DATE: 11/03/2000
 TIME: 12:09:40

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\11032000\I687860.raw

```

11 3 <110> APPLICANT: Asundi, Vinod
4      Ford, John E.
5      Drmanac, Radoje T.
6      Liu, Chenghua
7      Tang, Y. Tom
8      Yamasaki, Vicky
9      Yeung, George
10     Zhang, Jie
11     Zhou, Ping
13 <120> TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS
15 <130> FILE REFERENCE: 28110/36737
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/687,860
C--> 17 <141> CURRENT FILING DATE: 2000-10-13
17 <150> PRIOR APPLICATION NUMBER: US 09/620,312
18 <151> PRIOR FILING DATE: 2000-07-19
20 <150> PRIOR APPLICATION NUMBER: US 09/363,316
21 <151> PRIOR FILING DATE: 1999-07-28
23 <160> NUMBER OF SEQ ID NOS: 32
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 300
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)...(300)
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (1)...(300)
38 <223> OTHER INFORMATION: n = A,T,C or G
40 <400> SEQUENCE: 1
41   ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct      48
42   Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
43   1          5          10          15
45   gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt      96
46   Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
47   20          25          30
49   cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga      144
50   Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
51   35          40          45
53   atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc      192
54   Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
55   50          55          60
57   tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg      240
58   Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
59   65          70          75          80
W--> 61   tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt      288
W--> 62   Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys

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```

63                               85                               90                               95                               300
64 gaa gac aca gaa
65 Glu Asp Thr Glu
66                               100
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 1611
71 <212> TYPE: DNA
72 <213> ORGANISM: Homo sapiens
74 <220> FEATURE:
75 <221> NAME/KEY: CDS
76 <222> LOCATION: (1)...(1506)
78 <221> NAME/KEY: misc_feature
79 <222> LOCATION: (1)...(1611)
80 <223> OTHER INFORMATION: n = A,T,C or G
82 <400> SEQUENCE: 2
83 ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct 48
84 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
85 1 5 10 15
87 gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96
88 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
89 20 25 30
91 cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144
92 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
93 35 40 45
95 atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192
96 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
97 50 55 60
99 tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg 240
100 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
101 65 70 75 80
W--> 103 tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt 288
W--> 104 Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
105 85 90 95
107 gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc 336
108 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
109 100 105 110
111 cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc 384
112 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
113 115 120 125
115 tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt 432
116 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
117 130 135 140
118 gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc 480
119 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
120 145 150 155 160
122 agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc 528
123 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
124 165 170 175
127 cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc 576

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128	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	
129				180					185					190			
131	aag	tgt	aaa	tgc	aag	cag	gga	tat	aaa	ggc	aat	gga	ctt	cgg	tgt	tct	624
132	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	
133			195					200					205				
135	gct	atc	cct	gaa	aat	tct	gtg	aag	gaa	gtc	ctc	aga	gca	cct	ggt	acc	672
136	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	
137		210					215					220					
139	atc	aaa	gac	aga	atc	aag	aag	ttg	ctt	gct	cac	aaa	aac	agc	atg	aaa	720
140	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	
141	225				230					235					240		
143	aag	aag	gca	aaa	att	aaa	aat	gtt	acc	cca	gaa	ccc	acc	agg	act	cct	768
144	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	
145				245						250				255			
147	acc	cct	aag	gtg	aac	ttg	cag	ccc	ttc	aac	tat	gaa	gag	ata	gtt	tcc	816
148	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	
149			260					265					270				
151	aga	ggc	ggg	aac	tct	cat	gga	ggt	aaa	aaa	ggg	aat	gaa	gag	aaa	atg	864
152	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	
153		275					280						285				
155	aaa	gag	ggg	ctt	gag	gat	gag	aaa	aga	gaa	gag	aaa	gcc	ctg	aag	aat	912
156	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	
157		290				295					300						
159	gac	ata	gag	gag	cga	agc	ctg	cga	gga	gat	gtg	ttt	ttc	cct	aag	gtg	960
160	Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	
161	305				310					315				320			
163	aat	gaa	gca	ggt	gaa	ttc	ggc	ctg	att	ctg	gtc	caa	agg	aaa	gcg	cta	1008
164	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	
165			325					330					335				
167	act	tcc	aaa	ctg	gaa	cat	aaa	gat	tta	aat	atc	tgc	gtt	gac	tgc	agc	1056
168	Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	
169			340					345					350				
171	ttc	aat	cat	ggg	atc	tgt	gac	tgg	aaa	cag	gat	aga	gaa	gat	gat	ttt	1104
172	Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	
173		355					360					365					
174	gac	tgg	aat	cct	gct	gat	cga	gat	aat	gct	att	ggc	ttc	tat	atg	gca	1152
175	Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	
176		370				375					380						
178	gtt	ccg	gcc	ttg	gca	ggt	cac	atg	aaa	gac	att	ggc	cga	ttg	aaa	ctt	1200
179	Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	
180	385				390					395				400			
182	ctc	cta	cct	gac	ctg	caa	ccc	caa	agc	aac	ttc	tgt	ttg	ctc	ttt	gat	1248
183	Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	
184			405					410					415				
186	tac	cgg	ctg	gcc	gga	gac	aaa	gtc	ggg	aaa	ctt	cga	gtg	ttt	gtg	aaa	1296
187	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	
188			420				425						430				
190	aac	agt	aac	aat	gcc	ctg	gca	tgg	gag	aag	acc	acg	agt	gag	gat	gaa	1344
191	Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	

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192          435          440          445
194 aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc      1392
195 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
196          450          455          460
198 aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa      1440
199 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
200 465          470          475          480
202 atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc      1488
203 ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
204          485          490          495
W--> 206 ctt tta tct gtg gan nnc tgaatggtac tatctttata tttagactttg      1536
W--> 207 Leu Leu Ser Val Xaa Xaa
208          500
210 tatgtcagtt ccctgggtttt tttagatattg catcatagga cctctggcat tttaaaatta      1596
211 ctagctgaaa aattg      1611
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 100
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 3
219 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
220 1          5          10          15
221 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
222          20          25          30
223 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
224          35          40          45
225 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
226          50          55          60
227 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
228          65          70          75          80
229 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
230          85          90          95
231 Glu Asp Thr Glu
232          100
234 <210> SEQ ID NO: 4
235 <211> LENGTH: 537
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: VARIANT
241 <222> LOCATION: (1)...(537)
242 <223> OTHER INFORMATION: Xaa = Any Amino Acid
244 <400> SEQUENCE: 4
245 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
246 1          5          10          15
247 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
248          20          25          30
249 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
250          35          40          45

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```

251 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
252      50              55              60
253 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
254      65              70              75              80
255 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
256              85              90              95
257 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
258              100              105              110
259 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
260              115              120              125
261 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
262              130              135              140
263 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
264      145              150              155              160
265 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
266              165              170              175
267 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
268              180              185              190
269 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
270              195              200              205
271 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
272              210              215              220
273 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
274      225              230              235              240
275 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
276              245              250              255
277 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
278              260              265              270
279 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
280              275              280              285
281 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
282              290              295              300
284 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
285      305              310              315              320
286 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
287              325              330              335
288 Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
289              340              345              350
290 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
291              355              360              365
292 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
293              370              375              380
294 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
295      385              390              395              400
296 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
297              405              410              415
298 Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
299              420              425              430
300 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu

```

FWI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Pto.amc

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:416 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:416 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

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L:1295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1550 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29